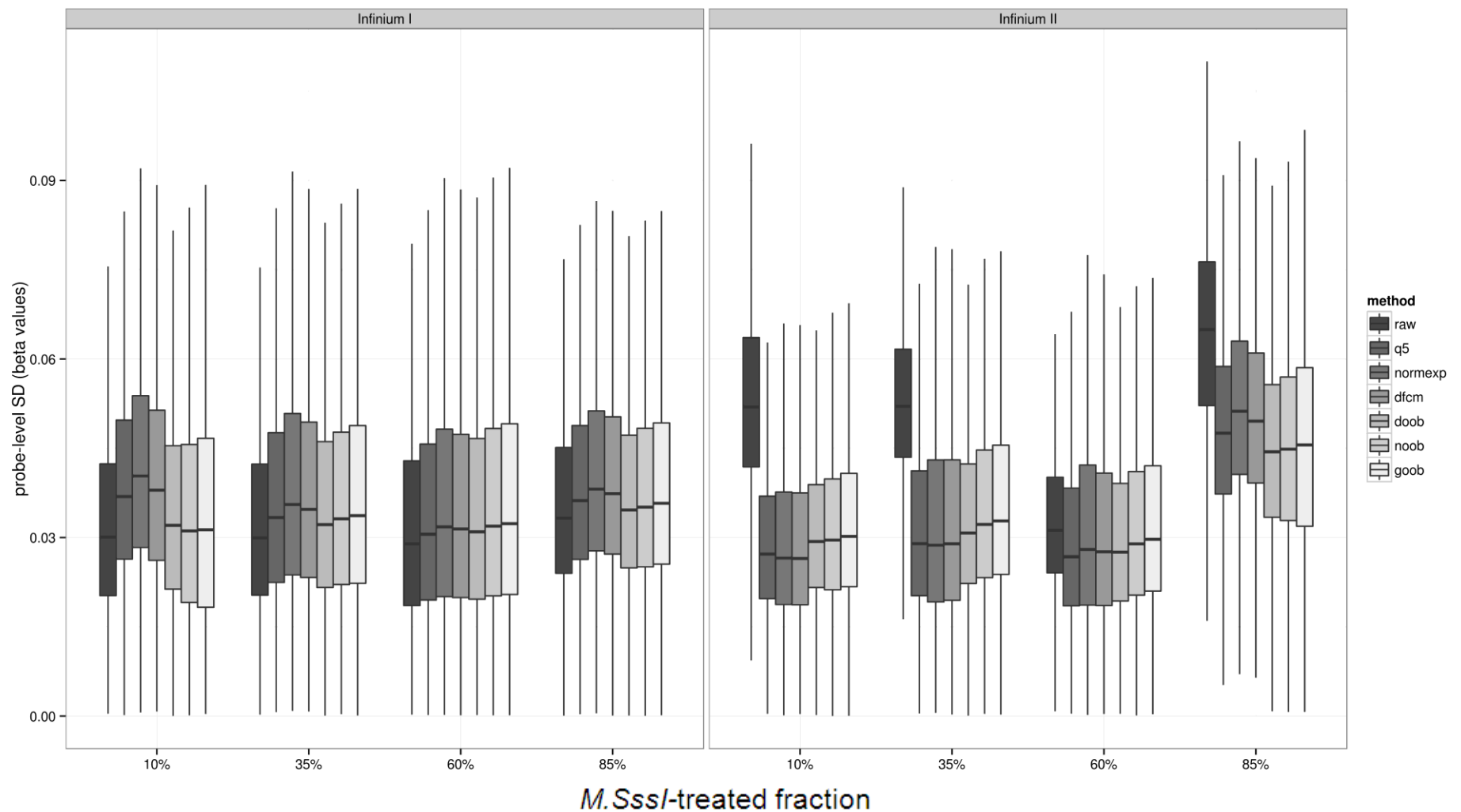Supplementary Figure 1 Q-Q plots of observed versus expected values for background and foreground intensities (left and right columns) in the green and red channel (top row and bottom row, respectively) for a randomly selected PBL sample. The out-of-band intensities from Infinium I probes appear in the left column (bg, background) and observed intensities from all probes (Infinium I and II) in the right (fg, foreground). The expected values for the foreground estimates are obtained by summing independent random variates from the the parametric convolutions (Gamma-gamma for goob, or Normal-exponential for noob). The horizontal dashed lines indicate the 5th and 95th percentiles of the observed data.
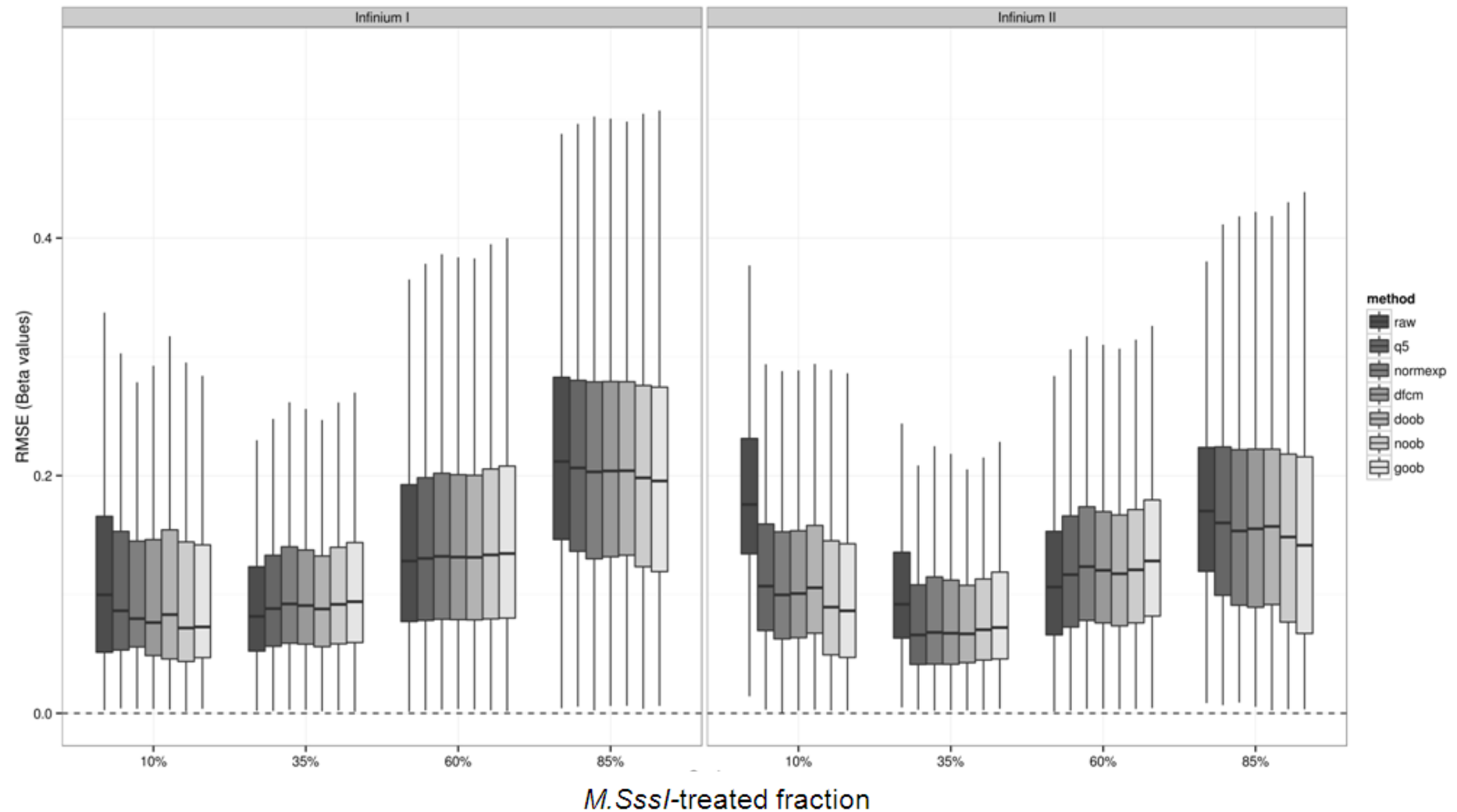
The plots of background intensity (left column) illustrate a better fit for the Gamma distribution (light color) than the Normal (dark) for points below the 95th percentile. For the observed intensities (right column), the estimates from the Gamma-gamma convolution (light) show a better fit than those from the Normal-exponential model (dark) for the middle 95% of the distribution.
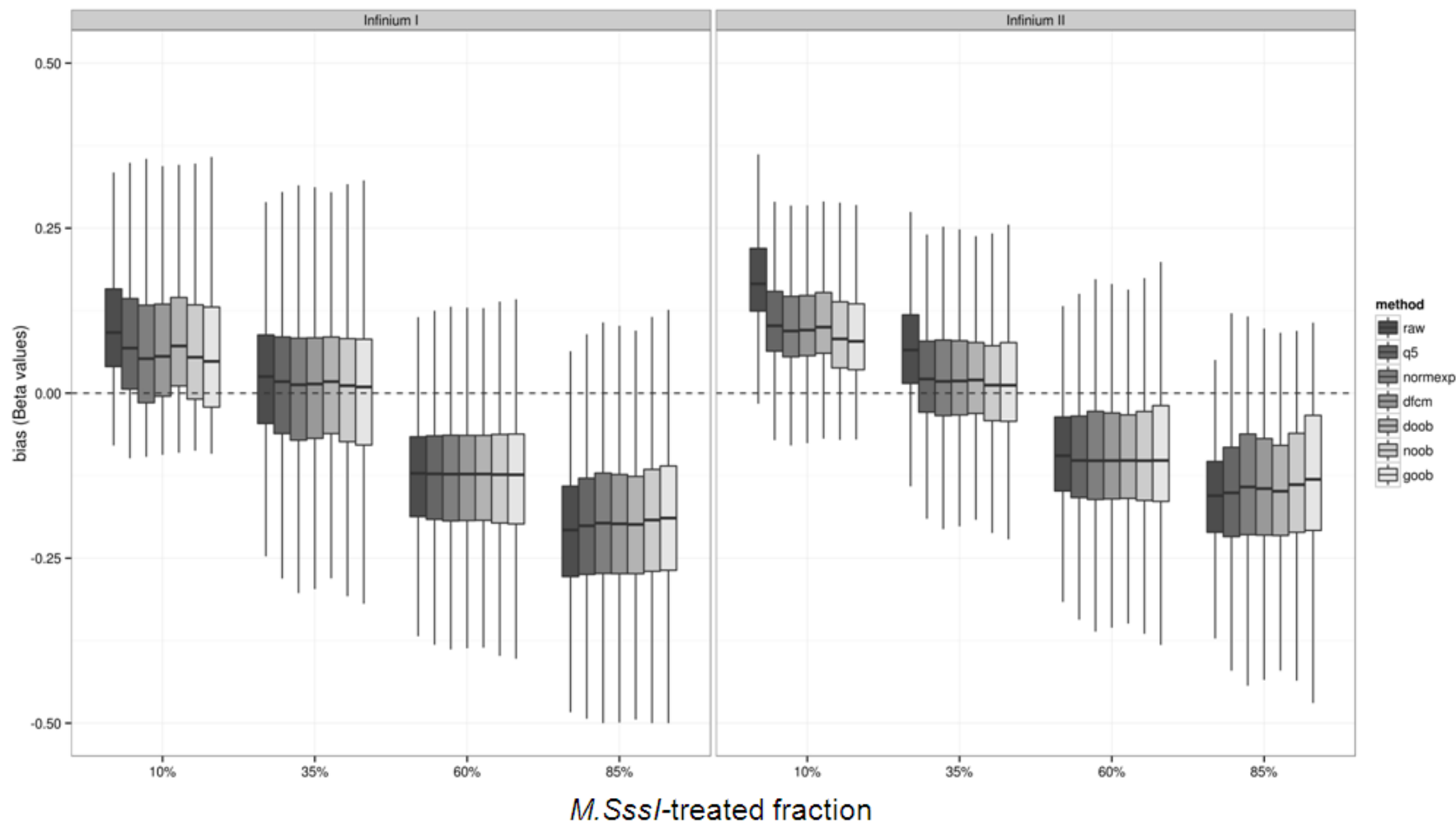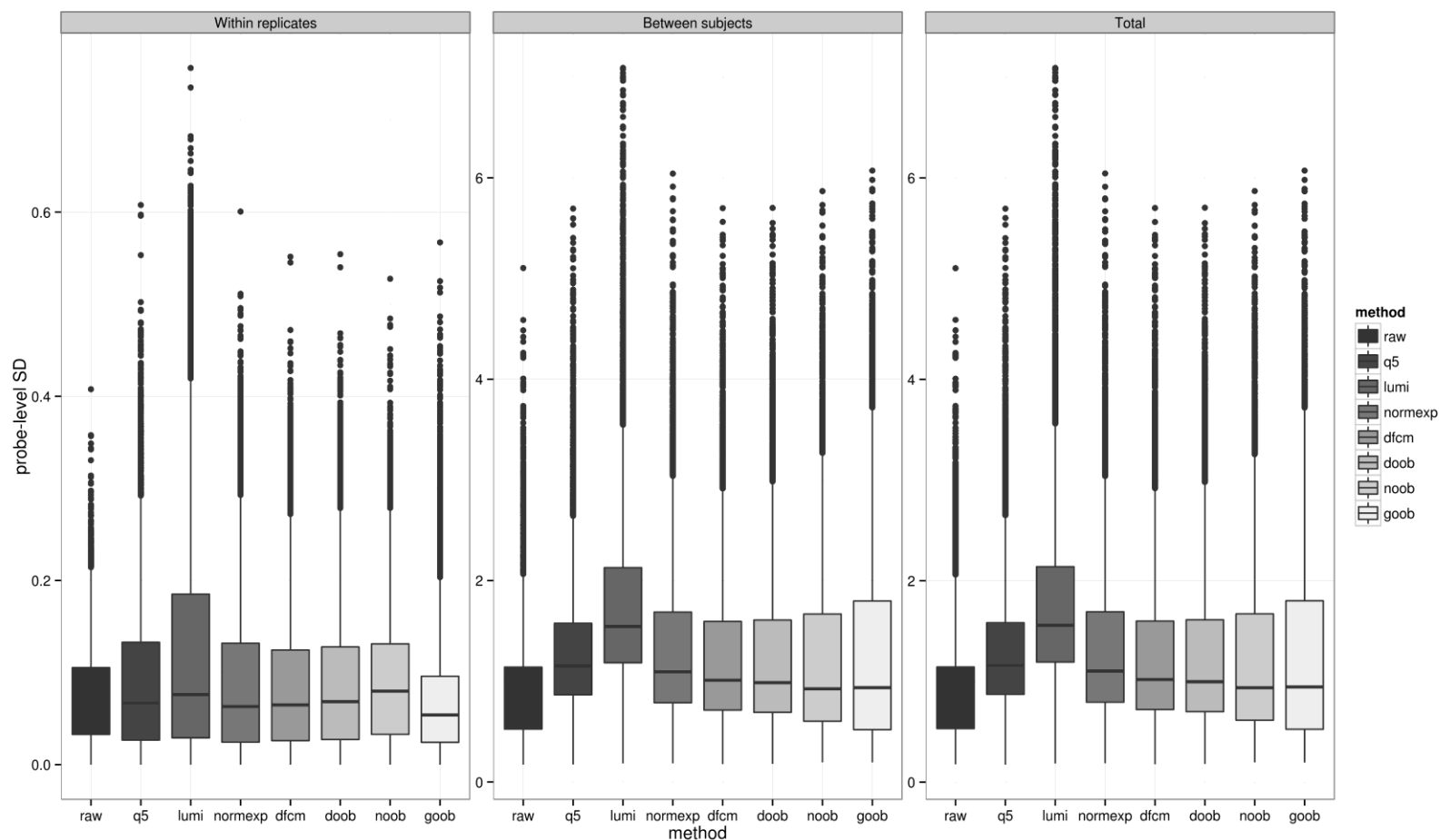
Supplementary Figure 2. Boxplot of probe-specific bias in Beta value by background correction method (left to right): none (raw), background subtraction using negative control probes (q5), Normal Exponential convolution using negative control probes (normexp), distribution-free convolution using negative control probes (dfcm), distribution-free convolution using out-of-band Infinium I probes (doob), Normal Exponential convolution using out-of-band Infinium I probes (noob), Gamma convolution using out-of-band Infinium I probes (goob). (N=4 replicates each of four mixtures samples, p=255,594 CpG targets, filtering out features methylated in the 10% M.*SssI*-treated fraction (Average Beta > 0.65)). Dye-bias equalization is also applied for all background corrected data, and probes are stratified by Infinium I and II design.
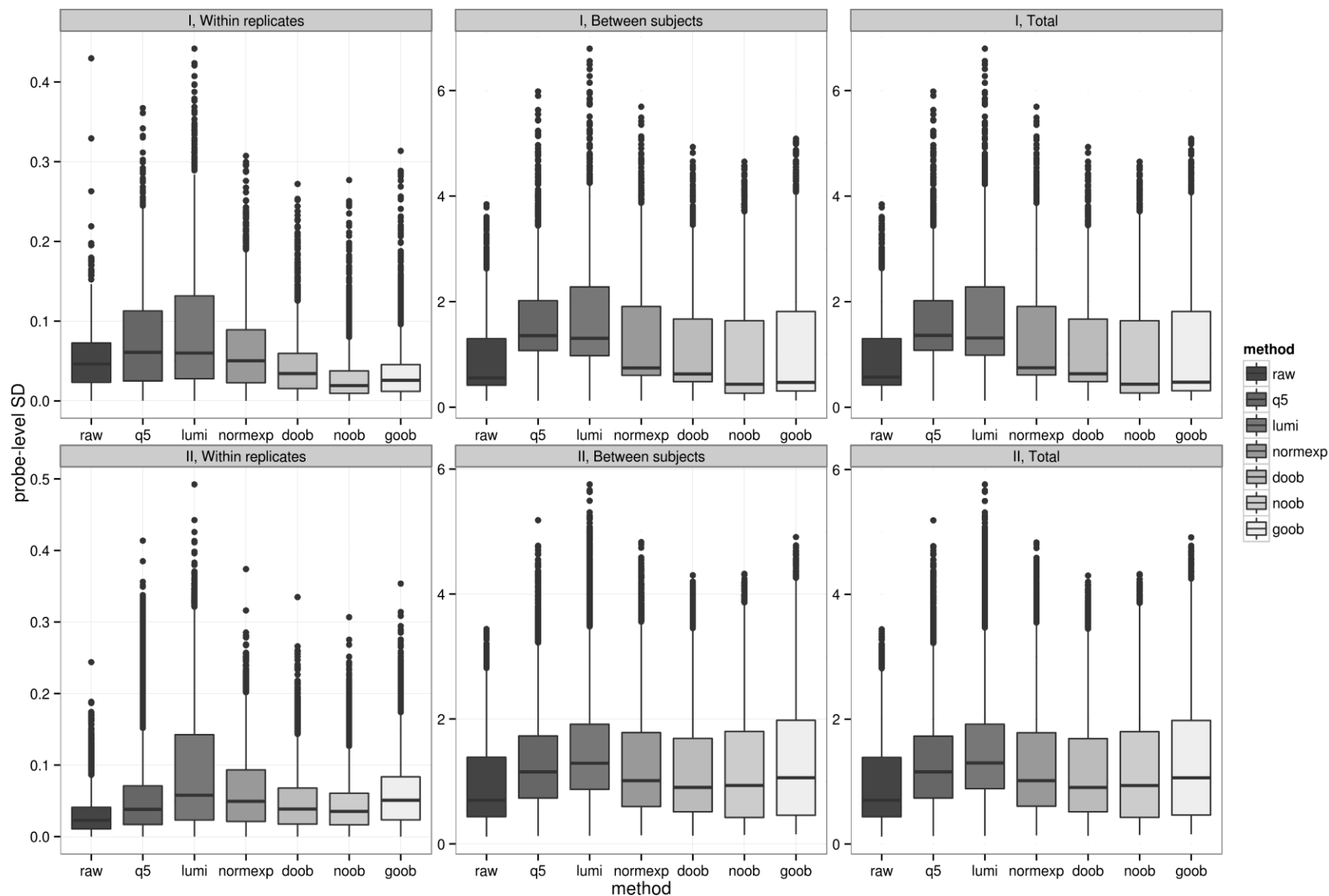
Supplementary Figure 3. Boxplot of probe-specific standard deviation of Beta value by background correction method (left to right): none (raw), background subtraction using negative control probes (q5), Normal Exponential convolution using negative control probes (normexp), distribution-free convolution using negative control probes (dfcm), distribution-free convolution using out-of-band Infinium I probes (doob), Normal Exponential convolution using out-of-band Infinium I probes (noob), Gamma convolution using out-of-band Infinium I probes (goob). (N=4 replicates each of four mixtures samples, p=255,594 CpG targets, filtering out features methylated in the 10% M.SssI-treated fraction (Average Beta > 0.65)). Dye-bias equalization is also applied for all background corrected data, and probes are stratified by Infinium I and II design.

Supplementary Figure 4. Boxplot of probe-specific root mean squared error of Beta value by background correction method (left to right): none (raw), background subtraction using negative control probes (q5), Normal Exponential convolution using negative control probes (normexp), distribution-free convolution using negative control probes (dfcm), distribution-free convolution using out-of-band Infinium I probes (doob), Normal Exponential convolution using out-of-band Infinium I probes (noob), Gamma convolution using out-of-band Infinium I probes (goob). (N=4 replicates each of four mixtures samples, p=255,594 CpG targets, filtering out features methylated in the 10% M.*SssI*-treated fraction (Average Beta > 0.65)). Dye-bias equalization is also applied for all background corrected data, and probes are stratified by Infinium I and II design.

Supplementary Figure 5: Boxplot of the probe-specific standard deviations of M-values within-subject, between-subject, and total, by background correction method: none (raw), background subtraction using negative control probes (q5), background subtraction using methylated allele intensities (lumi), Normal Exponential convolution using negative control probes (normexp), distribution-free convolution using negative control probes (dfcm), distribution-free convolution using out-of-band Infinium I probes (doob), Normal Exponential convolution using out-of-band Infinium I probes (noob), Gamma convolution using out-of-band Infinium I probes (goob). (N=160 HapMap samples).

Supplementary Figure 6: Boxplot of the probe-specific standard deviations of M-values on HM450 array by chemistry (I or II), within-subject, between-subject, and total, by background correction method: none (raw), background subtraction using negative control probes (q5), background subtraction using methylated allele intensities (lumi), Normal Exponential convolution using negative control probes (normexp), distribution-free convolution using negative control probes (dfcm), distribution-free convolution using out-of-band Infinium I probes (doob), Normal Exponential convolution using out-of-band Infinium I probes (noob), Gamma convolution using out-of-band Infinium I probes (goob). (N=192 TCGA AML samples). Dye-bias equalization is also applied for all background corrected data.